

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 05:25:38 ; Search time 2016.58 Seconds

(without alignments)
5946.845 Million cell updates/sec

Title: US-09-602-833a-1

Perfect score: 1116

Sequence: 1 atgagcacaataagtggtgtt.....cttttagccttaacttga 1116

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Database : EST

1: em_estfun:*
2: em_esthm:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estda:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: gb_estl:*
11: gb_estc:*
12: gb_hlc:*
13: gb_gss:*
14: gb_gss:*
15: em_gss_fun:*
16: em_gss_hum:*
17: em_gss_iny:*
18: em_gss_pln:*
19: em_gss_pro:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	812	72.8	1450	12	AK010252 Mus muscu
2	398.8	35.7	572	13	AO427239 CTTBI-EI-
3	384.6	34.5	560	10	AO427288 CTTBI-EI-
4	367.6	32.9	526	10	AA416235
5	323.2	29.0	483	10	AA422330 V538007.1
6	297.4	26.6	562	13	AO488137
7	250.6	22.5	453	13	AO791237 RPCI-11-2
8	246.6	22.1	557	10	BE110536 UI-R-BJ1-
9	237.4	21.3	462	13	AO729142 HS-5467.B
10	168	15.1	432	10	AA488294 UI-M-BH3-
11	167	15.0	443	10	AA500912 V903604.F
12	148.2	13.3	377	11	BG203142 RST22516

13	138	12.4	370	11	BG197958
14	137.8	12.3	598	13	AO670712 HS-5449.A
15	135	12.1	508	11	BG210970
16	125	11.2	470	10	AL120256
17	125	11.2	669	10	AL133928
18	119.6	10.7	244	10	BB563076
19	119.6	10.7	589	13	AZ412330
20	99	8.9	446	10	AA417843
21	91.4	8.2	470	13	AZ412322
22	86.8	7.8	366	10	AA446687
23	86.6	7.8	650	10	AA499431
24	83	7.4	794	10	AV700252
25	81.2	7.3	424	11	BG359014
26	76.4	6.8	194	10	AA149346
27	74.6	6.7	510	10	AW918885
28	72.4	6.5	370	10	AV690138
29	71.6	6.4	389	10	AA117972
30	70.4	6.3	798	12	AK008119
31	65.6	5.9	298	11	BF840611
32	64	5.7	377	10	AI399758
33	63.8	5.7	1245	12	AK006601
34	63.2	5.7	910	10	AL522572
35	60.4	5.4	490	11	BG736096
36	60.4	5.4	2026	12	AK017814
37	60.4	5.4	2085	12	AK011726
38	59.4	5.3	422	10	AA432896
39	59.4	5.3	450	11	BF545892
40	59.2	5.3	525	11	BF077050
41	57.4	5.1	826	11	BF344663
42	57.4	5.1	876	11	BG682195
43	56.4	5.1	772	10	AU123287
44	56.2	5.0	911	11	BG260067
45	55.8	5.0	691	10	AL138392

ALIGNMENTS

RESULT 1
AK010252
LOCUS
DEFINITION
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2400002D05, full insert sequence.
ACCESSION
AK010252
VERSION
AK010252.1 GI:12845555
KEYWORDS
CAP trapper.
SOURCE
Mus musculus (strain: C57BL/6J) ES cells cDNA to mRNA,
clone:1ib:RIKEN full-length enriched mouse cDNA library
clone:2400002D05.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1450)
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
METHODS in enzymology. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2 (bases 1 to 1450)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
METHODS in enzymology. 303, 19-44 (1999)
MEDLINE
20499374
PUBMED
11042159
REFERENCE
3 (bases 1 to 1450)
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Taashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,

Qy	1081	tataccaccacaaagtgtcctttagccctcaacttga	1116
Db	1234	TATAGACACCAAGTGTCAATTAGCTTTGAGCTTTGA	1269

RESULT	2
LOCUS	AO427239/c
DEFINITION	AO427239 572 bp DNA
ACCESSION	CITBI-El-2568B9.1R CITBI-El Homo sapiens genomic clone 2568B9, DNA
VERSION	AO427239.1
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens

TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
JOURNAL	Map Building
COMMENT	Unpublished (1997)
	Other_GSSS: CITBI-EL-256BB9.TF

Contact: Shanying Zhao, William Nierman, Mark Adams
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 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES	SOURCE
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/organism="Homo sapiens"	
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/clone_lib="CIRBI-E1"	
/sex="male"	
/cell_type="sperm"	
/note="Vector: pBeloBAC11; site_1: EcoRI; site_2: EcoRI; CalTech Human BAC Library D"	
BASE COUNT	134 a 157 c 104 g 177 t
ORIGIN	

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Best Local Similarity	85.8%;	Pred. NO. 8.9e-94;		
Matches 491; Conservative	0;	Mismatches 72;	Indels 9;	Gaps 4;

QY 38 tcaagcctctgtgggaaactcgtgtcaagaagcacaaagcttggagagaagaaggtg 97
|||||
Db 571 TCAGAGCCTTGTTGGGAAACTGTGTCAAAAAGCAC -AGTTTGGCAGAAAGAGGAGCG 513
QY 98 aaaggtcttgagaagaagcgcccttggagaagataaagagagatgtgaacttgtgcccgaat 157
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Db 512 AAAGCTTGGAAGAAAGGTGCATCATCAAAAAGACAAAGAGAGAGCGCCCTTGGGTCAACT 453
QY 158 gcaagaagaaggcgatcccccagagctgtgata-----ctgaagaatgagctctatagaca-- 211
|||||
Db 452 GCAGAGGAGGAAAGGCGCTTCCTCCTGGCTGAGTACTGGCTGGGATAGTGGCTTCTATGACATT 393
QY 212 -ccagctgtcgagctcttgagacaagatltgaagaaacactctcacaaagcagaattcaact 270
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Db 392 CATACGATGCAGGCTTCTGTGAAAGATAGAAAAGAAAGCTTCACAAAGCAGAGTTCACTT 333
QY 271 cccaagagcagaagcgaacagagcagtgctgttgtgttgaaactctbvgggagacatvg 330
|||||

Db	332	CCGAGGACGAGGACCAATGAGACAGTGTGTTGTGTTGGACCTTTCGGGAGTACTGG	273
Qy	331	acggagctccccaattcatttgaaagagcgacgaacaccgtagagaaatggtacataagaacat	390
Db	272	ACGGAGCTGCCAATTTGTTTAAAGGAGCGACCGACCTGTAGGAATGGCATGTATGGCAGC	213
Qy	391	acctgattcaaatccattccatatactatcagttatttccaagcgatagaattctgcat	450
Db	212	ACCTGATTCAAATTTACTCCACATATATATTGTAGCTGTGTTCAAGCGATGCAATTCAGAT	153
Qy	451	ctcgcaaaaaaccaatctcacatcttcacgaagaatcggltgtttgaagaacctgaaa	510
Db	152	CTGCGCAAGAAAPAAATCTCACATTTTCCAGCTTAACACAGTTGTTTGAAGAACCTGAAA	93
Qy	511	gaactcaatitggttttctaactatactgaagagcattctccagaattggaattgtgaa	570
Db	92	TAACTCAATGTGAGTTTCAACTATCTGGAAGACATTTCTCCAGACTGGAGATTGTG- A	34
Qy	571	aattctagagagatgattgtttctggaact	602
Db	33	AATCTAGAGGAGCTGAGTTGTTCTGGAAATCT	2

RESULT	3				
LOCUS	AO427288/c				
DEFINITION	citrbl-el-25680D1.TR citrbl-el Homo sapiens genomic clone 2568D1, DNA				
ACCESSION	AO427288	560 bp	DNA	GSS	24-MAR-1999
VERSION	AO427288				
KEYWORDS	AO427288.1	GI:4500038			
SOURCE	human.				

ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 560)				
Zhao, S., Adams, M.D., Niernan, W., Malek, J., Shizuya, H., Simon, M. and				
Venter, J. C.				
Use of BAC End sequences from Caltech Libraries for Sequence-Ready				
Map Building				
Unpublished (1997)				
Other_GSSs: CITBI-El-2568D1.TF				

Contact: Shaying Zhao, William Niernan, Mark Adams
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9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetjgr.Org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hunngen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

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FEATURES
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1..560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568D1"
/clone_1b="CITBI-E1"
/sex="male"
/cell_type="sperm"
/notes="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human PAC Library D"
BASE COUNT
132 a
154 c
101 g
173 t

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Best Local Similarity	85.2%;	Pred. No. 4,6e-90;		
Matches 478;	Conservative	0;	Mismatches 74;	Indels 9;
			Gaps	4;
0y	49	tgggaactcgtgtcaagaagcacaagaagcttggcagaagaagagttggaagcgttgag	108	

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Db      560  TGGGAACCTGTGTCAAGAGCAC-TAGTTGGCAGAAAGAGCGCAAAAGCTTTAG 502
Qy      109  aagagcgcccttgagaagataaaggagtggaacttctgtgcccgaatgcagaggaag 168
Db      501  AAGATGCATCATGAAAAGCAAGAGAGAGTGCCCTTGAGCTGACATGACGAGAGAA 442
Qy      169  ggcaccccccaagctgtata---ctgcaagaatggtctcatagaca---ccagctgag 221
Db      441  GGCACTCTCTGGCTGAGACTGCTGGATGAGTGCTTCATAGACATTCATAGCATGCA 382
Qy      222  gctcttgacaagaattgaaagaacactctcaaggcgaagttcaacttcccaagacaag 281
Db      381  GCTTGTGAAAAGATAGAAAAGAGAGCTTCACAAAGCAGAGTCTCCCAAGAGACG 322
Qy      282  aggcacaagcagcagctgctgttcttgaaacttctgaggagacacgagcagctccc 341
Db      321  AGGCAAAATGAGACACTGTGTGTTGTTGAGACTTCTGGGAGTACTGAGACGAGACTGC 262
Qy      342  agatcattgaagagcagacacacctgagagaatggtacataagaacataactgattca 401
Db      261  AGATTGTTAAAGAGAGACAGACGACCTGAGAGATGCAATGATGTCGACACCCGTATTCA 202
Qy      402  aatcctccatataatcagttatttccaagcagtgagaattctgagatctgcacaaaa 461
Db      201  AATTACTCCACATATATATGAGCTGTTCAACGATGAGAAATTCAGATCTGCCAAAGAA 142
Qy      462  ccaactccacactctcagcagaagaatcggtgtctggaagaacccgaaagaacatagt 521
Db      141  ACAATTCACATTTTCCAGCTAAACTCAGTTGTTGAAGAACCTGAAATTAATCAATCT 82
Qy      522  ggggttbaatctgaagagagctctcaggaattgagagatctgaaatctagagag 581
Db      81  GATTTCAACTATCTGAAGAGCATCTCCAGAGCTGGAGATGTG-AAATCTAGAGG 23
Qy      582  actgagtgtctggaatct 602
Db      22  ACTGATGTTCTGGAATCT 2

RESULT 4
AA416235 526 bp mRNA EST 16-OCT-1997
LOCUS v138b07.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:846037
DEFINITION 5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-I GENE PRODUCT ; mRNA sequence.
ACCESSION AA416235
VERSION AA416235
KEYWORDS GI:2076503
SOURCE EST.
ORGANISM house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 526)
Marras, S., Kucaba, T., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Mashu-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:498189
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 482.

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                /clone_lib="Soares mouse NBMH"
                /sex="male"
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                /lab_host="DHI0B"
                /note="vector: pT73D-Pac (Pharmacia) with a modified
                polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was primed with a Not I - 01190(dt) primer (5'
                TGTTCACCAATCTGAAAGTGGAGCGCGCGGACGAAATGTTTTTTTTTTTTT
                3'); double-stranded cDNA was ligated to Eco RI adaptors
                (pharmacia), digested with Not I and cloned into the Not
                I and Eco RI sites of the modified pT733 vector. RNA
                provided by Dr. Minoru Ko, Wayne State Univ. Library
                constructed and normalized by Bento Soares and M.Palma
                Bonaldo."
BASE COUNT 140 a 122 c 130 g 134 t
ORIGIN
Query Match 32.9%; Score 367.6; DB 10; Length 526;
Best Local Similarity 81.2%; Pred. No. 1.3e-85;
Matches 427; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 520 gtgggttccaactactgaagaagcattccctcagaagttggagatgtgaaatcctaag 579
Db 1 gtgacttttaaccatttaaaagatatttccccggagctgagactgtgacatctagag 60
Qy 580 agactggaattctcgaatactagaataatgagcgcgccttgaaatgaatctg 639
Db 61 agactggaattctcgaatactagaataatgagcgcgccttgaaatgaatctg 120
Qy 640 aagcaagttacattttagatatactcagaacaagaatttccagtgctcccaattg 699
Db 121 AAGCAAGTTACATTTGTGATATCTCTCGAACAAGTTCTCCAGCGTTCATCTGTGTC 180
Qy 700 ctggagtgatggaatttcaatggtgtgatatcagcaacaataactcagcagctggcg 759
Db 181 ctggcgatgtgcgtctcagagtgctgatatccacacacaaacatctagcactgcca 240
Qy 760 caagatatacagcagctagagagcgtgcagagccttctctgtatataaacaagttag 819
Db 241 CAAGATATAGACAGGCTGGAAGAGCTACAGAGTTCCGTGCTGATTAATAACAAGCTGAC 300
Qy 820 taacttccattccaatgctgaacctgaagaagctcactctgtagtcgtcagtgaggac 879
Db 301 TACCTTCTTCAAGCATCTCAACCTCAAAAAGCTCACCTTGCTGCTGAGTGGGAT 360
Qy 880 catttggtgaggtccccaacgctgctgtgatactcattcacaacacttaaatgttag 939
Db 361 CACTGTGGAGAGTCCACGCGCCCTTGCGATGCTCTCAAGCCCTTTAAATTTGTAGC 420
Qy 940 ctatgagacaatctcattgataatgccaatgtggaatggaatggaatggaatggaat 999
Db 421 CTTGTGACAAATCCCATTTGATTAAGACCGGATGTAACAAGACTGAAGACAGTGAAGAGC 480
Qy 1000 gaaeggagatgcacaacatttgataaagaagttatgaagcctata 1045
Db 481 GAGCGGAGCGCCGACGATTTGATTAAGAAATTTAAGAACATATA 526

RESULT 5
AA422330 483 bp mRNA EST 16-OCT-1997
LOCUS v145b09.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:846713
DEFINITION 5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-I GENE PRODUCT ; mRNA sequence.
ACCESSION AA422330

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REFERENCE	TITLE	COMMENT	FEATURES
AA22330.1	GI:2101146		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 483)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
	The WashU-HMNI Mouse EST Project		
	Unpublished (1996)		
	Contact: Marra M/Mouse EST Project		
	WashU-HMNI Mouse EST Project		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: mouseest@wustl.edu		
	This clone is available royalty-free through LLNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	MG1:498865		
	Seq primer: -28m13 rev2 EF from Amesham		
	High quality sequence swap: 479.		
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	/dev_stage="4 weeks"		
	/lab_host="DH10B"		
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	was primed with a Not I - oligo(dT) primer [5',		
	TGTTACCAATCTGTGAAGGAGGAGCGCGCGAAAGTTTCTTTTCTTTTCTTTT		
	3']; double-stranded cDNA was ligated to Eco RI adaptors		
	(Pharmacia), digested with Not I and cloned into the Not		
	I and Eco RI sites of the modified pT73 vector. RNA		
	constructed by Dr. Minoru Ko, Wayne State Univ. Library		
	constructed and normalized by Bento Soares and M.Fatima		
	Bonaldo."		
BASE COUNT	125 a 115 c 120 g 123 t		
ORIGIN			
Query Match	29.0%; Score 323.2; DB:10; Length 483;		
Best Local Similarity	80.6%; Pred. No.5.2e-74;		
Matches 390; Conservative 0; Mismatches 93; Indels 1; Gaps 1;			
QY 520	gtgggttcaactatctgaagacatctctccagaatgtagagattgtgaaatctagag 579		
Db 1	GTGAGTTTAAACATTGTAAGAGTATTC-CGGAGCTAGGAGACTGTGACATCTAGAG 59		
QY 580	agaactgatttctctggaactctagaatctaatgtagcgtcccttgaattgaattg 639		
Db 60	AGACGTGACCTGTCTGGGAATCTGCACTGTGATGTGATCCCTTGAATTAAGTAAATTG 119		
QY 640	aagcaagttaacttgtgatctatctcagcaaaagaatttccagtggtcccaatctgtgc 699		
Db 120	AAGCAAGTTACATTTGTGTGATATCTCTCGAACAAGTTCTCCAGCGTTCATCTGTGTC 179		
QY 700	ctgcgagtgatcgaattctcagtggttgatataccagcagaataaactcagcagctgcg 759		
Db 180	CTGCGGATGTGTGCTGTCTGCAATGCGGTGTGATATCACACACAACATCTAGTACTGCCA 239		
QY 760	caagatatacagcagctagagagagcttcgtagcagcttctctgtataaaacaagtgtacc 819		

Db	240	CAAAATATTAGACAGCGCTGGAGAGGCTACAAAGGTTTCTCTCTATTATAAAAACAAGCTGACC	299
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Db	300	TACCTTCCTCAAGCGACATCTCAACCTCAAAAGCCTCACCTTGCTGTTGTTCAGTGGGAT	359
QY	880	cattgtgtgagctcccaactgcctctgtgtgactatccacacctttaaatltgtaacg	939
Db	360	CACCTGGTGAGGCGCCGACCGCCCTCTGGAGAGCCTCCACGCCCTTGGAAATTTGTAAGC	419
QY	940	ctttggacaatcctattgataatgtcccaattggaagatgagcaatgaaataatgtgaagt	999
Db	420	CTGTGGACATTCACATTGATTAAGACCGGATGTCAAGACACTGAAGACACACTAGAGAGC	479
QY	1000	gaac 1003	
Db	480	GAGC 483	
RESULT	6		
AQ488137/c	AQ488137	562 bp	DNA
LOCUS	RPCT-11-264L9	TV	RPCT-11 Homo sapiens genomic clone RPCT-11-264L9,
DEFINITION	DNA sequence.		
ACCESSION	AQ488137		
VERSION	AQ488137.1	GI:4674011	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (phases 1 to 562)		
	Zhao, S., Adams, M. D., Nierman, W., Malek, J., de Jong, P. and Venter, J. C.		
TITLE	Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready Map Building		
JOURNAL	Unpublished (1997)		
COMMENT	Other.GSS: RPCT-11-264L9.TU		
	Contact: Shaying Zhao, William Nierman, Mark Adams		
	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850		
	Tel: 301 838 0200		
	Fax: 301 838 0208		
	Email: hbe@ligr.org		
	Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong		
	BAC/CPC Resources (http://bacpac.med.buffalo.edu). Clones may be purchased from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tc/b/hungen/bac_end_search/bac_end_search.html.		
	Seq primer: T7		
	Class: BAC ends.		
FEATURES	Location/Qualifiers		
source	1..562		
	/organism="Homo sapiens"		
	/db_xref="GDB:7601264"		
	/db_xref="taxon:9606"		
	/clone="RPCT-11-264L9"		
	/clone_11b="RPCT-11"		
	/sex="Male"		
	/cell_type="Lymphocytes"		
	/note="Vector: pBAC3.6; site.1: EcoRI; site.2: EcoRI; RPCT11 Human Male BAC Library"		
BASE COUNT	122 a 152 c 119 g 165 t		
ORIGIN			
Query Match	26.6%;	Score 297.4;	DB 13; Length 562;
Best Local Similarity	83.5%;	Pred. No. 3e-67;	Indels 8; Gaps 3
Matches 375; Conservative	0;	Mismatches 66;	
1 atggagcaataaagtgtgtgtcttcgacatttcgtcatcagaagcctgttg99aactcgt 60			

D	b	448	ATGGGATATCAAAAGTGGTCATATTTTGACATTTCTGTGTCAAGCCTTGTGGAAACCTTGT	388
Q	Y	61	gtcaagaagcacaagctcttgacagaagaaggttgaaagcttgaagagcgcccttg	120
D	b	388	GTCAAGAAGCAC - AAGTTTGGCAGAAAGAGGAGGCAGAAAGTCTTGAGAAAGATGCATCA	330
Q	Y	121	gagaagataaagaagaagtgaactctgtgcccgaatgcaggaagaaggcatccccag	180
D	b	329	GAAGAAACAAGGAGGAGGTGGCCCTTGAGTCAAGTGCAGAGAGAAAGGCAATCTCTGG	270
Q	Y	181	gctctata----ctgcaagaatlgcttcatagaa----cgaagtgaggttctcgcgaa	233
D	b	269	GCTAGTACTGCTGGGATGATGGCTTCATPAGATTCATPAGCATGAGCTTCGTGGAAA	210
Q	Y	234	gattgaagaagacactctccacaagaagagttcaactcccaagaagacagaagcaagag	293
D	b	209	GATGAAAGAAAGAACTCTCACMAAGCAGATTCATCTCCCAAGACACAGAGCAAAATGAG	156
Q	Y	294	cagtgcttctgttcttgaacttcttgaggagcacttgcagagctgcccaattcatgaa	353
D	b	149	CAGTGTGTTTGTGTTGGACTTCTTGGGAGTACTGGACGAGCTGCCAGATTGTTAAA	90
Q	Y	354	ggagcagaacacacctgagagaaatggtacataagcaataaccttgattcaaatcatcttac	413
D	b	89	GGACACAGACGCACTTGAGAGATGGCATGTAATCGACACACCTGATTCAAATTAATCTCCAC	30
Q	Y	414	atatattcagttattttaaaggaatgaana 442	
D	b	29	ATAATATGAGCTGTTTCAAGGATGAGAAA 1	

RESULT	7
A0791237/c	
LOCUS	A0791237 453 bp DNA
DEFINITION	H8_5495_A2_F06_T7A Rpci-11 Human Male BAC Library Homo sapiens
ACCSSION	g genomic.C10ne.Plate=1071 Col=12 Row=K, DNA sequence.
VERSION	A0791237
KEYWORDS	A0791237.1 GI:5698784 GSS.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE AUTHORS	TITLE
1 (bases 1 to 453) Mahairas,G.G., Wallace,J.C., Smith,R., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589	Contact: Mahairas GG, Wallace JC, Hood L

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@ejon.med.buffalo.edu). Clones may be purchased from BACPC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end Web Server: <http://www.hnsc.washington.edu>
Plate: 1071 row: K column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 453.

FEATURES	Location/Qualifiers
source	1. .453
	/organism="Homo sapiens"
	/db_xref="taxon:9606"

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/clone="Plate=1071 Col=12 Row=R"
/clone.lib="RPCr-11 Human Male BMC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRII Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT      116 a      108 c      78 g      146 t      5 others
ORIGIN

```

Query Match	22.5%	Score 250.6	DB 13	Length 453
Best Local Similarity	83.6%	Pred. No. 5.1e-55		
Matches 305	Conservative 0	Mismatches 58	Indels 2	Gaps 2
QY 229	gacaagattgaaagaaacactctcacaagcgagatctacttcccaaggacagsgcaaa	288		
DB 402	GAAGAATGAAAGAAAGCTCTCACAAGCGAGATTCTCCCAAGGACAGAGCGCAA	343		
QY 289	cgagacagtggtgtttgtttgtaacctcttggggagcaactggaagagctccacgatcca	348		
DB 342	TGGAGCATTGATTGTGTGTGTAACCTTCCTGGGAGTACTAAAGGAGCTCCAGATTG	283		
QY 349	ttgaagagcgacagacacacctgagagaatggtacataagcaataccttgatccaatcat	408		
DB 282	TTATAGAGCGAGACGACACTTGAGAGAAATGCGATTATGCGACACCATGATTCAAATTACT	223		
QY 409	ccatacatatctcagttattccaagcgatgagaattctgtaactgtgcccataaaccaaatc	468		
DB 222	CCCCACATTATTGGAGCTGTTTCCAAGCGATGAGATTCTCGCAATCAACCAATTC	163		
QY 469	tcaactcttccaagaagaatcggtgtgtttgagaagaacctgaaagaactcaatgctggttc	528		
DB 162	TCACATTTTCCAGCTAAACCTCAGTTGTTTGAAGAACTTAAATATATCAATGTAAGTTTC	103		
QY 529	aactacttgaagagcatctcctccagaatttggagaatttggaaaactctagagagaagct	588		
DB 102	TACTATGTGAAGA-AAAAAACCAGAGACTGCGACAGTTGTG-NNATCTCFAGAGGAGTGAGT	45		
QY 589	tgctc 593			
DB 44	TGTCC 40			

RESULT	8
BEL10536/c	
LOCUS	BEL10536
DEFINITION	BE110536 557 bp mRNA EST 13-JUN-2000
ACCESSION	U1-R-BJ1-avt-b-09-0-U1 s1 U1-R-BJ1 Rattus norvegicus cDNA clone
VERSION	U1-R-BJ1-avt-b-09-0-U1 3' , mRNA sequence.
KEYWORDS	BE110536 BE110536 GI:8502641
SOURCE	EST.
ORGANISM	Norway rat.
	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 557)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
JOURNAL	discovery Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	Contact: Soares, MB

Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: meoares@blue.weeg.uiowa.edu
The sequence contained an oligo-AT track that was present in the
oligonucleotide that was used to prime the synthesis of first

Db 300 TTGTGACTACGACCTTAAATTTGTAAGCTTATAACATCC 348

RESULT 10
 AM488294/c 432 bp mRNA EST 24-FEB-2000
 LOCUS AM488294
 DEFINITION UI-M-BH3-ary-h-06-0-UT.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
 ACCESSION AM488294
 VERSION AM488294.1 GI:7058564
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 432)
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704447
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mbs@emil.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hippocampus library cDNA library preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 1-32, >AT-richlow.complexity
 Seg primer: M13 forward
 POLY-A=yes.

FEATURES

source

Location/Qualifiers
 1. 432
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH3-ary-h-06-0-UT"
 /clone_id="NIH_BMAP_M_S4"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT7AD-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography.

converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG-LIB=NIH_BMAP_M_S4
 TAG-TISSUE=hippocampus
 TAG_SEQ=TCGA*

BASE COUNT 118 a 85 c 83 g 145 t 1 others
 ORIGIN

Query Match 15.1%; Score 168; DB 10; Length 432;
 Best Local Similarity 82.4%; Pred. No. 2.1e-33;
 Matches 192; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 431 TGGTGAGGTCGACCGCCCTTGTGCGTCACGCCCTTGAAATTTGAAGCCTTG 372
 Oy 944 tggacaatccatgataatgccaatgtgaagatggaatgaataatggaagtgaac 1003
 Db 371 TGGACAATCCCATGTGATTAAGACCGGATGTCAAGACACTGAAGACACAGTAGAGCGAGC 312
 Oy 1004 gggatcgccaacatttgataaagaagtatgaagactatattgaagacttaagaa 1063
 Db 311 GGGACCGCCACGATTTGATTAAGAAATTTATGAAGCATTAATTTGAAGACCTTAAGAA 252
 Oy 1064 gagatcgtgtccagcagctacacccaagaagtgcttttagcctcaacttga 1116
 Db 251 GAGAACTGTTCCCAAGTTATACGACCAAGTGTATTAGTCTTACGACTTTGA 199

RESULT 11
 AA500912 443 bp mRNA EST 01-JUL-1997
 AA500912
 LOCUS vq03064.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:860263
 DEFINITION 5', mRNA sequence.
 ACCESSION AA500912
 VERSION AA500912.1 GI:2235879
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 443)

REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:504351

FEATURES
 source
 Putative full length read
 vector to vector length is
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 362.
 Location/Qualifiers

1. 443
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:860263"


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/clone_lib="Soares mouse NDMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/pole="vector; pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTTACCAATCTGACAGTGGAGCGCCGCCGAATTTTTTTTTTTTTTTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Felma
Bonaldo."

```

	Query Match	15.0%	Score 167	DB 10	Length 443
	Best Local Similarity	80.8%	Pred. No. 3,8e-33		
	Matches 219	Conservative 0	Mismatches 50	Indels 2	Gaps 2
OY	848	agaagctcaactctgttagtcgltcagltgaggaccattggtgga-gctcccaactgcctt	906		
Db	1	AAAAGCTCACCTTGGTGGTTGTCAAGTGGGGATACACTGTATGACGGTCCCGACCCCTTC	60		
OY	907	tgtaactcatccacacaccttaaaatttgaagcctatggaacacctctatgataatgcc	966		
Db	61	TGCGATGCTTCACGCCCTTTGAATTTTAAOCTTTTGACAAATCCATTATATAAGCC	120		
OY	967	caatgtgaagaatggcaatgaaataatggaagtgaacggatgcgcaac-atttgataa	1025		
Db	121	GGAGTGTCAAGCACCTGAAAGCACAGTAAAGAGCGGAGCCGACCCACAGATTTTGATPA	180		
OY	1026	agaagtatgaaagcctatcttgaagacctaaagaagaagaatctgttcccaagctaac	1085		
Db	181	GGATTTTATGAAGCATTTATTTGAAGACCTTAAAGAAAGAGAGAGTGTTCACAGTTATAC	240		
OY	1086	caaccaagtgctctttagagccttcaacttga	1116		
Db	241	GACCAAAAGTGTATTAGTCTTCAGCTTTGA	271		

RESULT	12				
LOCUS	BG203142				
DEFINITION	BG203142	377 bp	mRNA	EST	21-Apr-2001
ACCESSION	R5722516	Athersys RAGE Library	Homo sapiens	cDNA, mRNA	sequence.
VERSION	BG203142				
KEYWORDS	BG203142.1	GI:13724829			
SOURCE	EST.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 377) Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,T., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Krashoc,D., McElligott,K., Clair,S., Mays,R., Smith,E., Veloso,N., Hess,J., Cochran,K., Lo,K., Offenbacher,J., Danzig,J. and Ducat,M. Creation of genome-wide Protein Expression Libraries using Random Activation of Gene Expression Nat. Biotechnol. 19 (5), 440 (2001) In press Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scai@atersys.com High quality sequence stop: 377. Location/Qualifiers 1..377				

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athensys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

```

	Query Match	Similarity	13.3%	Score 148.2	DB 11	Length 377
	Best Local	Similarity	96.6%	Pred. No. 3e-28		
	Matches	172	Conservative	0	Mismatches	4
					Indels	2
					Gaps	2
QY	939	ccttatgagacatccctatagtataatgcccattgtaagaatgycgaatgaataatggaag	998			
Db	16	CTTGAGNACAATCTATTGTAATATGCC - ATGTAGAG - GGCATGGAATATGGAAG	73			
QY	999	tgaacggatctgcgaacatttggataaagaagtatgaagccctatattgaagacctta	1058			
Db	74	TGAACGGATCGCCACATTTTGTATGAAGAGATTTGTGAAGCCCTATTATGAGAGACCTTAA	133			
QY	1059	agaagaagaatcgtctccagatatacaaccagaatgctctttagccttcaacttga	1116			
Db	134	AGAAGAACAATCTGTTCCAGCTATACCAACCAAGTGTCTTTAGCTTCAACTTTGA	191			

RESULT	13
LOCUS	BGI97958
DEFINITION	BGI97958 370 bp mRNA
ACCESSION	RS117210
VERSION	BGI97958
KEYWORDS	EST.
SOURCE	BGI97958.1 GI:13719645
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 370)
	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Cochren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE	Creation of genome-wide Protein Expression Libraries using Random Activation of Gene Expression
JOURNAL	Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT	Contact: Scott J. Cain
	Athersys, Inc.
	3201 Carnegie Ave, Cleveland, OH 44115, USA
	Tel: 216 431 9900
	Fax: 216 361 9596
	Email: scaine@atersys.com
	High quality sequence stop: 324.
FEATURES	Location/Oualifiers
source	1..370
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_lib="Athersys RAGE Library"
	/cell_line="HT1080"
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT	137 a 65 c 63 g 104 t 1 others
ORIGIN	

Query Match 12.4%; Score 138; DB 11; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 979 ggcattgaatgaagtgagcgcgcacacatttgataagagattatgaa 1038
 |||||||
 Db 48 ggcattgaatgaatgaagtgagcgcgcacacatttgataagagattatgaa 107

Qy 1039 ggcattgaagccttaagaagaagatctgttccagctataccacaaagtgtct 1098
 |||||||
 Db 108 ggcattgaatgaagccttaagaagaagatctgttccagctataccacaaagtgtct 167

Qy 1099 tttagcctcaacttga 1116
 |||||||
 Db 168 tttagcctcaacttga 185

RESULT 14
 A0670712 598 bp DNA GSS 24-JUN-1999
 LOCUS HS_5449_A2_E11_T7A RPCR-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=1025 Col=22 Row=1, DNA sequence.
 ACCESSION A0670712
 VERSION A0670712.1 GI:5203458
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

JOURNAL 99380589
 MEDLINE
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCR-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.washington.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.washington.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 1025 row: 1 column: 22
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 598.

FEATURES
 Location/Qualifiers
 source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=1025 Col=22 Row=1"
 /clone_lib="RPCR-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites" 8 others

BASE COUNT 185 a 97 c 121 g 187 t
 ORIGIN

Query Match 12.3%; Score 137.8; DB 13; Length 598;
 Best Local Similarity 92.4%; Pred. NO. 1.8e-25;

Matches 145; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 928 aaatttgagccttatgacacatctatgataatgcacaaatggaatgcaatgaa 987
 |||||||
 Db 181 AGATTGTGAACCTTATGACCAATCCTATTGATAATGCCCAATGGAATGCCAATGA 240

Qy 988 ataatgagaatgagcggatcgccacacatttgataagaagtataagaccatatt 1047
 |||||||
 Db 241 ATAATGGAAGTGAACGGGATCGCCACATTTTGAATAAGAGATTATGAAGCCTTAAT 300

Qy 1048 gaagacccttaagaagaagatctgttccagctata 1084
 |||||||
 Db 301 GAAGACCTTAAGAAGAGGTGGTGTACTCATATCTA 337

RESULT 15
 BG210970 508 bp mRNA EST 21-APR-2001
 LOCUS R8730524 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG210970
 VERSION BG210970.1 GI:13732657
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
 Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.,
 and Ducar,M.
 Creation of Genome-wide Protein Expression Libraries using Random
 Activation of Gene Expression
 Nat. Biotechnol. 19 (5), 440 (2001) In press
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com

JOURNAL
 MEDLINE
 COMMENT Activation of Gene Expression
 Nat. Biotechnol. 19 (5), 440 (2001) In press
 Contact: Scott J. Cain

FEATURES
 Location/Qualifiers
 source
 1..508
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 182 a 81 c 83 g 160 t 2 others
 ORIGIN

Query Match 12.1%; Score 135; DB 11; Length 508;
 Best Local Similarity 98.1%; Pred. No. 9.3e-25;
 Matches 157; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 957 tgataatgccaatgtaagatgcaatgaaataatggaagatgaacggatgcgaaca 1016
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 Db 33 TGNATATGCCCAATGTG-AGATGCAATGAAT-ATGGAAGTGAACGGATGCCCAACA 90

Qy 1017 tttagataaagaattatgaaagccttatgaaagccttaagaagaagatgtgttc 1076
 |||||||
 Db 91 TTTTGATTAAGAAAGCTTATGAAGGCTTATGAAGACCTTAAGAAGAGATCTGTCC 150

Qy 1077 cagctaccacacaaagtgtcttttagcctcaacttga 1116
 |||||||
 Db 151 CAGCTATACCAACCAAGTGTCTTTTACGCTTCAACTTTGA 190

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Job time: 16313 sec
